SUBSTITUTE SEQUENCE LISTING

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ISHII, Hideshi

<120> COMPOSITIONS, KITS, AND METHODS RELATING TO THE HUMAN FEZ1 GENE, A NOVEL TUMOR SUPPRESSOR GENE

<130> 9855-30U1 (209855.0081)

<140> NOT YET ASSIGNED
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<150> US 60/121,537
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<212> PRT
<213> Homo sapiens

<400> 4
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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385 390 395 400

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Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
                405                 410                 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420                 425                 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
        435                 440                 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
    450                 455                 460

Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala
465                 470                 475                 480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp
                485                 490                 495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Arg Ala Glu Leu Arg
            500                 505                 510

Glu Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu
        515                 520                 525

Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys
    530                 535                 540

Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu
545                 550                 555                 560

Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro
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Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile
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Ala Thr Glu Ile
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<212> PRT
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<400> 5

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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
        35                  40                  45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
    50                  55                  60
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Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg Arg
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<211> 69
<212> PRT
<213> Homo sapiens

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20 25 30

Leu Gln Val Leu Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu
35 40 45

Leu Glu Ser Leu Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg
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Ser Tyr Glu Arg Glu
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<210> 7
<211> 68
<212> PRT
<213> Homo sapiens

<400> 7
Ile Ser Arg Arg Arg Arg Glu Lys Glu Asn Pro Lys Glu Arg Asn Lys
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Met Ala Ala Ala Lys Cys Arg Asn Arg Arg Arg Glu Leu Thr Asp Thr
20 25 30

Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln
35 40 45

Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile
50 55 60

Leu Ala Ala His
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<210> 8
<211> 69
<212> PRT
<213> Homo sapiens

<400> 8
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Leu Gln Gln Val Ala Arg Arg Ala Gln Arg Ala Gln Gln Gly Leu Gln
             20                  25                  30

Leu Gln Val Leu Arg Leu Gln Gln Asp Lys Lys Gln Leu Gln Glu Glu
         35                  40                  45

Ala Ala Arg Leu Met Arg Gln Arg Glu Glu Leu Glu Asp Lys Val Ala
     50                  55                  60

Ala Cys Gln Lys Glu
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<210> 10
<211> 633
<212> DNA
<213> Homo sapiens

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<210> 11
<211> 1614
<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<211> 1692
<212> DNA
<213> Homo sapiens

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<211> 1722
<212> DNA
<213> Homo sapiens

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tcccagacgg aggtgaacgc caaggctagc gagatcctgg gtctcaaggc acagctgaag 1260
gacacgcggg gcaagctgga gggcctggag ctgaggaccc aggacctgga gggcgccctg 1320
cgcaccaagg gcctggagct ggaggtctgt gagaatgagc tgcagcgcaa gaagaacgag 1380
gcggagctgc tgcgggagaa ggtgaacctg ctggagcagg agctgcagga gctgcgggcc 1440
caggccgccc tggcccgcga catggggccg cccaccttcc ccgaggacgt ccctgccctg 1500
cagcgggagc tggagcggct cgtgtggaag gaggagaagg agaaggtgat tcagtaccag 1560
aaacagctgc agcagagcta cgtggccatg taccagcgga accagcgcct ggagaaggcc 1620
ctgcagcagc tggcacgtgg ggacagcgcc ggggagccct tggaggttga cctggaaggg 1680
gctgacatcc cctacgagga catcatagcc actgagatct ga 1722

<210> 15
<211> 76
<212> PRT
<213> Homo sapiens

<400> 15
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
35 40 45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
50 55 60

Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg Arg
65 70 75

<210> 16
<211> 210
<212> PRT
<213> Homo sapiens

<400> 16
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln

```
         35                  40                  45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
     50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65                  70                  75                  80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
                 85                  90                  95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
            100                 105                 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
        115                 120                 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130                 135                 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145                 150                 155                 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
                165                 170                 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Ala Gly Glu Pro Leu Glu
            180                 185                 190

Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr
        195                 200                 205

Glu Ile
    210


<210> 17
<211> 537
<212> PRT
<213> Homo sapiens

<400> 17
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1               5                  10                  15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
             20                  25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
         35                  40                  45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
     50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65                  70                  75                  80
```

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
370 375 380

```
Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385                 390                 395                 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
                405                 410                 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420                 425                 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
        435                 440                 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
    450                 455                 460

Arg Glu Lys His Glu Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val
465                 470                 475                 480

Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln
                485                 490                 495

Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp
            500                 505                 510

Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro
        515                 520                 525

Tyr Glu Asp Ile Ile Ala Thr Glu Ile
    530                 535


<210> 18
<211> 504
<212> PRT
<213> Homo sapiens

<400> 18
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1               5                  10                  15


His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
             20                  25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
         35                  40                  45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
     50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65                  70                  75                  80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
                 85                  90                  95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
```

```
            100                 105                 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
        115                 120                 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130                 135                 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145                 150                 155                 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
                165                 170                 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
            180                 185                 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
        195                 200                 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
    210                 215                 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225                 230                 235                 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
                245                 250                 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
            260                 265                 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
        275                 280                 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
    290                 295                 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305                 310                 315                 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
                325                 330                 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
            340                 345                 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
        355                 360                 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
    370                 375                 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385                 390                 395                 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
```

```
                405                 410                 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420                 425                 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
        435                 440                 445

Val Cys Glu Asn Glu Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg
    450                 455                 460

Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser
465                 470                 475                 480

Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr
                485                 490                 495

Glu Asp Ile Ile Ala Thr Glu Ile
            500
```

<210> 19
<211> 563
<212> PRT
<213> Homo sapiens

<400> 19

```
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1               5                  10                  15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
             20                  25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
         35                  40                  45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
     50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65                  70                  75                  80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
                 85                  90                  95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
            100                 105                 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
        115                 120                 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130                 135                 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145                 150                 155                 160
```

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
435 440 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
450 455 460

```
Arg Glu Lys Val Asn Leu Leu Glu Arg Leu Arg Ala Glu Leu Arg Glu
465                 470                 475                 480

Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu Arg
                485                 490                 495

Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln
            500                 505                 510

Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu
        515                 520                 525

Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu
    530                 535                 540

Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala
545                 550                 555                 560

Thr Glu Ile
```

<210> 20
<211> 573
<212> PRT
<213> Homo sapiens

<400> 20

```
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1               5                  10                  15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
             20                  25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
         35                  40                  45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
     50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65                  70                  75                  80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
                 85                  90                  95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
            100                 105                 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
        115                 120                 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130                 135                 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
```

```
145                 150                 155                 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
                165                 170                 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
            180                 185                 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
        195                 200                 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
    210                 215                 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225                 230                 235                 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
                245                 250                 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
            260                 265                 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
        275                 280                 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
    290                 295                 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305                 310                 315                 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
                325                 330                 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
            340                 345                 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
        355                 360                 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
    370                 375                 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385                 390                 395                 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
                405                 410                 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420                 425                 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
        435                 440                 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
```

```
    450                 455                 460

Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala
465                 470                 475                 480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp
                485                 490                 495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Val Trp Lys Glu Glu
            500                 505                 510

Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val
        515                 520                 525

Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu
    530                 535                 540

Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly
545                 550                 555                 560

Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr Glu Ile
                565                 570
```

<210> 21
<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: F37 Probe

<400> 21
ggactctgcc cctggacctg ggaacgactg gactgtcacg gggttccctc ctagctctcc 60
cagtgaactc ctgccaggca cacacagccc ctatagcact gagctcacat gggactggga 120
tatgggggca tctcttcccc agagaggcac tcagtgagcc tcctgtgcct ggccccagtc 180
tgggccatct cttaggtgag acagttgccc gaaactaagc caggcctggc tggaggagca 240
gcagcttggg gagagggatt tccctgcaga cctcaagcca tcatgcggtg ggtgctgcca 300
tgacagaggc tgcacccctg ggccagcggg gctgctcacc cacctcttgt gcaaggtggc 360
ctttgtgctg cgcctgcagg cagagctgga gcccccagca gaggcaggct gggacggacc 420
agcatctgga agatgtacat agttattttt ctctttgtgg tttcttgttt ggtttggttt 480
gcttttgaca gcttcatttt atttttgacg tcacttttg gccatgtaaa ctatttgtgg 540
caattttatg tttttattta tgaataaaga atgccatttc tcacgccctc t 591

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplificatin primer G12

<400> 22
gctgccacag cctttccaag acc 23

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplificatin primer G13

<400> 23
taccggttga gcttcttgag gtg 23

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G14.2

<400> 24
acagcttcca cagcaagcac tgc 23

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G15

<400> 25
attggagaag ggcatgagct t 21

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G16

<400> 26
tggactttga cccgtccaca cc 22

<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer IntABR

<400> 27
gtttccaacc cacttaccct tgc 23

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer IntABF

<400> 28
gcaggggagg catgagtcac c 21

<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G17

<400> 29
ggcttcagct cctgctcctt gg 22

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G20

<400> 30
acaacatcac ccagggcatc gtc 23

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G21

<400> 31
cctccagctc gtccctgcag c 21

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G32

<400> 32
actgcagctt cagcaggaga agc 23

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer IntBCR

<400> 33
ctgaccaccc aaacccatga gc 22

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer IntBCF

<400> 34
tcacctcttg gcactctgtc tcc 23

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer Mut6

<400> 35
caggtcctgg gtcctcagct c 21

<210> 36

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G1

<400> 36
tgaacgccaa ggctagcgag atc 23

<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G2

<400> 37
gctcctgcag ctcctgctcc ag 22

<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G75

<400> 38
cccaccttcc ccgaggacgt c 21

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G82

<400> 39
agcccgagga catctggtca tgg 23

<210> 40
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G5

<400> 40
cctgccctgc agcgggagct ggag 24

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G6

<400> 41
agctgctgca gggccttctc cag 23

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G7

<400> 42
cagtaccaga aacagctgca gcagagc 27

<210> 43
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable region amplification primer G8

<400> 43
ccctgcctcc cagtgccagg tc 22

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: First strand of partially-double stranded adapter-linker

<400> 44
gatctcgacg aattcgtgag acct 24

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Second strand
of partially-double stranded adapter-linker

<400> 45
tggtctcacg aattcgtcga 20

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 46
tcccaggact ccggtcacgg caa 23

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 47
gagcggcaag gccatgacca g 21

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 48
agcctgccca cacacagcac cag 23

<210> 49
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 49
cagcgccggg gagcccttgg a 21

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 50
gtgagaatga gctgcagcgc aag 23

<210> 51
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 51
cagcagagct acgtggccat gt 22

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 52
agctgctgcg ggagaaggtg aac 23

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 53
cagcatgagc ggctcgtgtg ga 22

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site sequence of truncated FEZ1 truncation region

<400> 54
aggtgaacct gctggagcag gag 23

<210> 55
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site sequence of truncated FEZ1 truncation region

<400> 55
gagcggctgc gggccgagct gc 22

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site sequence of truncated FEZ1 truncation region

<400> 56
ctgcagcggg agctggagcg gctg 24

<210> 57
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site sequence of truncated FEZ1 truncation region

<400> 57
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<210> 58
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for amplifying FEZ1 cDNA

<400> 58
cagatgggca gcgtcagtag cctcatc 27

<210> 59
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for amplifying FEZ1 cDNA

<400> 59
tcagatctca gtggctatga tgtc 24

<210> 60
<211> 8073
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide sequence of vector pQBI-AdCMV5-IRES-GFP

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Example

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<210> 62
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<212> DNA
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<223> Description of Artificial Sequence: Example

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<210> 63
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<212> DNA
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<223> Description of Artificial Sequence: Example

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<223> Description of Artificial Sequence: Example

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